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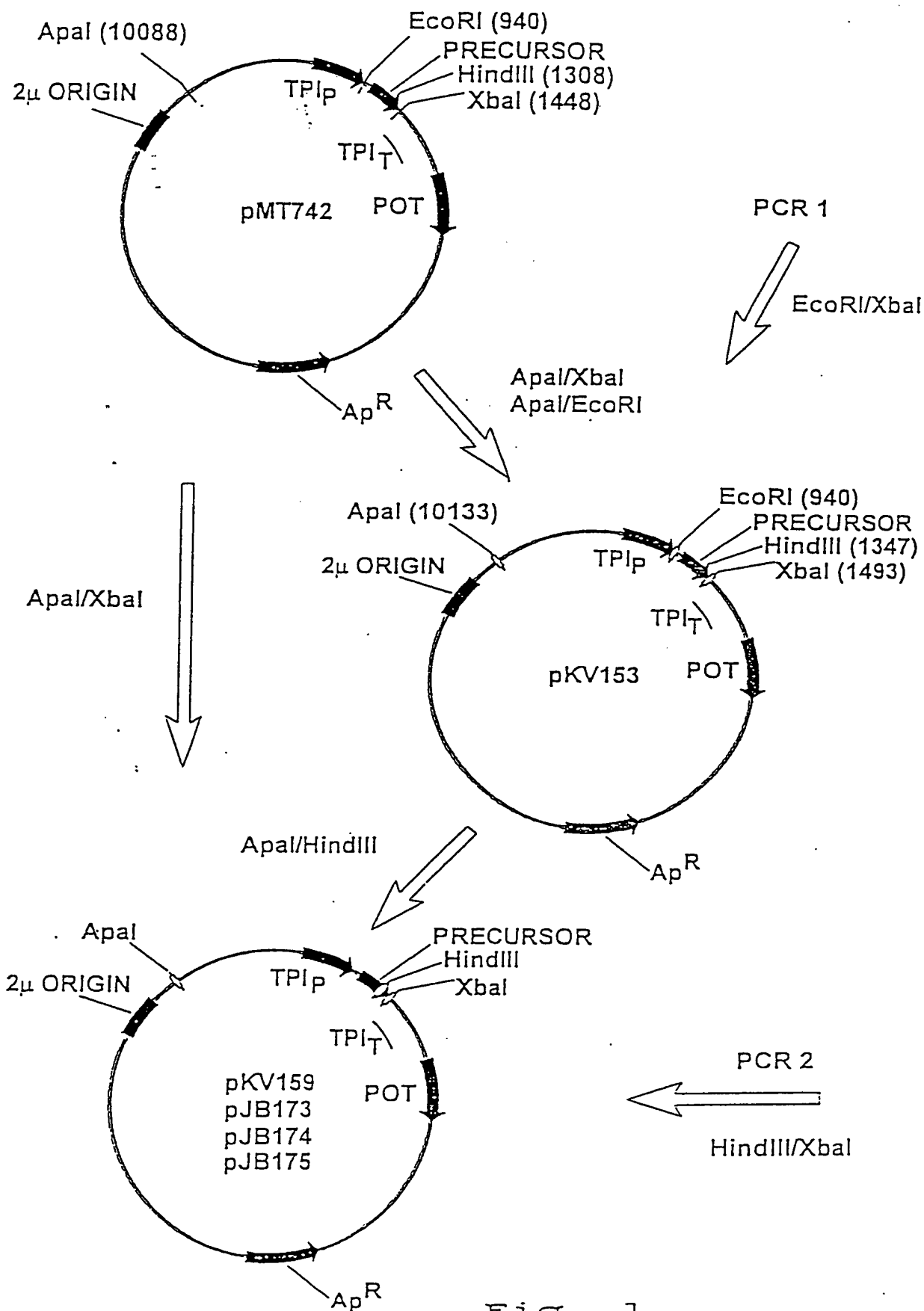


Fig. 1

#94 1

5' -TAAATCTATAACTACAAAAACACATA-3' EcoRI

5' -CTTAAATCTATAACTACAAAAACACATACAGGAATTCCATTCAAGAATAGTTCAAACAA

907 ---+-----+-----+-----+-----+-----+-----+-----+----- 966

3' -GAATTTAGATATTGATGTTTTTTGTGTATGTCCTTAAGGTAAGTTCTTATCAAGTTTGTT

GAAGATTACAACTATCAATTTTCATACACAATATAAACGATTAAAAGAATGAGATTTCTCT

967 ---+-----+-----+-----+-----+-----+-----+-----+----- 1026

CTTCTAATGTTTGATAGTTAAAGTATGTGTTATATTTGCTAATTTTCTTACTCTAAAGGA

MetArgPhePro 4

TCTATTTTACTGCTGTTTTATTTCGCTGCTTCCTCCGCTTTAGCTGCTCCAGTCAACACT

1027 ---+-----+-----+-----+-----+-----+-----+-----+----- 1086

AGATAAAAATGACGACAAAATAAGCGACGAAGGAGGCGAAATCGACGAGGTCAGTTGTGA

SerIlePheThrAlaValLeuPheAlaAlaSerSerAlaLeuAlaAlaProValAsnThr 24

ACCACTGAAGATGAAACGGCTCAAATTCCAGCTGAAGCTGTCATCGGTTACTCTGATTTA

1087 ---+-----+-----+-----+-----+-----+-----+-----+----- 1146

TGGTGACTTCTACTTTGCCGAGTTTAAGGTCGACTTCGACAGTAGCCAATGAGACTAAAT

ThrThrGluAspGluThrAlaGlnIleProAlaGluAlaValIleGlyTyrSerAspLeu 44

GAAGGTGATTTTCGATGTTGCTGTTTTGCCATTTTCCAACCTCCACCAATAACGGTTTATTG

1147 ---+-----+-----+-----+-----+-----+-----+-----+----- 1206

CTTCCACTAAAGCTACAACGACAAAACGGTAAAAGGTTGAGGTGGTTATTGCCAAATAAC

GluGlyAspPheAspValAlaValLeuProPheSerAsnSerThrAsnAsnGlyLeuLeu 64

TTTATCAATACTACTATTGCCTCCATTGCTGCTAAAGAAGAAGGTGTTTCTTTGGATAAA

1207 ---+-----+-----+-----+-----+-----+-----+-----+----- 1266

AAATAGTTATGATGATAACGGAGGTAACGACGATTTCTTCTCCACAAAGAAACCTATTT

PheIleAsnThrThrIleAlaSerIleAlaAlaLysGluGlyValSerLeuAspLys 84

3' -CCACAAAGAAACCTATTT

HindIII

5' -TTGGTTGAAGCTTTGTACTTGGTTTGC

1267 ---+-----+-----+-----+-----+-----+-----+-----+----- 1326

AGATTGCTTAACCAACACTTGTGCGGTTCCCACTTGGTTGAAGCTTTGTACTTGGTTTGC

TCTAAGCAATTGGTTGTGAACACGCCAAGGGTGAACCAACTTCGAAACATGAACCAAACG

ArgPheValAsnGlnHisLeuCysGlySerHisLeuValGluAlaLeuTyrLeuValCys 104

TCT GCAATTGGTTGTGAACACGCCAAGGGTGAACCAACTTCGAAACATGAACC-5'

C A #593 1

T ATGTAGCCTTTGGT

T T TGACGATGCT

CTTCGACTTCGACTTCGAC C A

#3075 1 T G

GGTGAAGAGGTTTCTTCTACACTCCTAAG AGGTATTG-3'

1327 ---+-----+-----+-----+-----+-----+-----+-----+----- 1386

GGTGAAGAGGTTTCTTCTACACTCCTAAGGCTGCTAAGGGTATTGTCGAACAATGCTGT

CCACTTTCTCCAAAGAAGATGTGAGGATTCGACGATTCCCATACAGCTTGTTACGACA

GlyGluArgGlyPhePheTyrThrProLysAlaAlaLysGlyIleValGluGlnCysCys 124

ACCTCCATCTGCTCCTTGTACCAATTGGAAAACCTACTGCAACTAGACGCAGCCCCGAGGC

1387 ---+-----+-----+-----+-----+-----+-----+-----+----- 1446

TGGAGGTAGACGAGGAACATGGTTAACCTTTTGATGACGTTGATCTGCGTCGGGCGTCCG

ThrSerIleCysSerLeuTyrGlnLeuGluAsnTyrCysAsn*** 3' -GGGCGTCCG 138

Fig. 2a

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XbaI
1447 TCTAGAACTAAGATTAATATAATTATATAAAAAATATTATCTTCTTTCTTTAT-3'
-----+-----+-----+-----+-----+-----+
AGATCTTTGATTCTAATTATATTAATATATTTTATAATAGAAGAAAAGAAATA-5'
AGATCTTTGATTCTAATT-5'
#2371 ! 1500

Fig. 2b